



SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Mc Wherter, Charles  
Feng, Yiqing  
Mc Kearn, John  
Staten, Nicholas  
Streeter, Philip  
Woulfe, Susan  
Minster, Nancy  
Minnerly, John

(ii) TITLE OF THE INVENTION: Circular Permuteins of FLT3 Ligand

(iii) NUMBER OF SEQUENCES: 151

(iv) CORRESPONDENCE ADDRESS:  
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(D) STATE: Texas  
(E) COUNTRY: USA  
(F) ZIP: 77002

(v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: CD  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: DOS  
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: Unknown  
(B) FILING DATE: 20-AUG-2003  
(C) CLASSIFICATION: Unknown

(vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: US 08/955,090  
(B) FILING DATE: 21-OCT-97

(viii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 60/030,094  
(B) FILING DATE: 25-OCT-1996

(ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 713-276-5383  
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(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 135 amino acids

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- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ala Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe  
1 5 10 15  
Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro  
20 25 30  
Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Ala Leu  
35 40 45  
Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr Val  
50 55 60  
Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile  
65 70 75 80  
His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu Arg  
85 90 95  
Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln  
100 105 110  
Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys  
115 120 125  
Leu Glu Leu Gln Cys Gln Pro  
130 135

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ala Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe  
1 5 10 15  
Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro  
20 25 30  
Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Leu  
35 40 45  
Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr Val  
50 55 60  
Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile  
65 70 75 80  
His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu Arg  
85 90 95  
Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln  
100 105 110  
Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys  
115 120 125  
Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu  
130 135 140

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid

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(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ala Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe  
1 5 10 15  
Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro  
20 25 30  
Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly Leu  
35 40 45  
Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr Val  
50 55 60  
Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile  
65 70 75 80  
His Phe Val Thr Lys Cys Ala Phe Gln Glu Thr Ser Glu Gln Leu Val  
85 90 95  
Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu  
100 105 110  
Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu  
115 120

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 135 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Gly Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe  
1 5 10 15  
Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro  
20 25 30  
Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly Leu  
35 40 45  
Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr Val  
50 55 60  
Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile  
65 70 75 80  
His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu Arg  
85 90 95  
Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln  
100 105 110  
Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys  
115 120 125  
Leu Glu Leu Gln Cys Gln Pro  
130 135

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 140 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Gly Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe  
1 5 10 15  
Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro  
20 25 30  
Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly Leu  
35 40 45  
Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr Val  
50 55 60  
Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile  
65 70 75 80  
His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu Arg  
85 90 95  
Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln  
100 105 110  
Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys  
115 120 125  
Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu  
130 135 140

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ala Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe  
1 5 10 15  
Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro  
20 25 30  
Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly Leu  
35 40 45  
Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr Val  
50 55 60  
Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile  
65 70 75 80  
His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu Arg  
85 90 95  
Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln  
100 105 110  
Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys  
115 120 125  
Leu Glu Leu Gln Cys Gln Pro  
130 135

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ala Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe  
1 5 10 15  
Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro  
20 25 30  
Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly Leu  
35 40 45  
Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr Val  
50 55 60  
Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile  
65 70 75 80  
His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu Arg  
85 90 95  
Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln  
100 105 110  
Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys  
115 120 125  
Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu  
130 135 140

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ala Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln  
1 5 10 15  
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly  
20 25 30  
Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala  
35 40 45  
Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser  
50 55 60  
Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp  
65 70 75 80  
Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro  
85 90 95  
Asp Ser Ser Thr Leu Ser Gly Gly Asn Gly Ser Gly Gly Asn Gly Ser  
100 105 110  
Gly Gly Asn Gly Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser  
115 120 125  
Ser Asp Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln  
130 135 140  
Asp Tyr Pro Val Thr Val Ala Ser Asn Leu Gln  
145 150 155

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

Seq List 10-644355.txt

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Ala Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln  
1 5 10 15  
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly  
20 25 30  
Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala  
35 40 45  
Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser  
50 55 60  
Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp  
65 70 75 80  
Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro  
85 90 95  
Asp Ser Ser Thr Leu Ser Gly Gly Asn Gly Ser Gly Asn Gly Thr  
100 105 110  
Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val  
115 120 125  
Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr  
130 135 140  
Val Ala Ser Asn Leu Gln  
145 150

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ala Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln  
1 5 10 15  
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly  
20 25 30  
Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala  
35 40 45  
Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser  
50 55 60  
Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp  
65 70 75 80  
Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro  
85 90 95  
Asp Ser Ser Thr Leu Ser Gly Gly Asn Gly Thr Gln Asp Cys Ser Phe  
100 105 110  
Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu  
115 120 125  
Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu  
130 135 140  
Gln  
145

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid

Seq List 10-644355.txt

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Ala Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile His  
1 5 10 15  
Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe  
20 25 30  
Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu  
35 40 45  
Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu  
50 55 60  
Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Ser Gly Gly Asn Gly  
65 70 75 80  
Ser Gly Gly Asn Gly Ser Gly Gly Asn Gly Thr Gln Asp Cys Ser Phe  
85 90 95  
Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu  
100 105 110  
Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu  
115 120 125  
Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln  
130 135 140  
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly  
145 150 155

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 150 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ala Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile His  
1 5 10 15  
Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe  
20 25 30  
Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu  
35 40 45  
Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu  
50 55 60  
Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Ser Gly Gly Asn Gly  
65 70 75 80  
Ser Gly Gly Asn Gly Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile  
85 90 95  
Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu  
100 105 110  
Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu  
115 120 125  
Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg  
130 135 140  
Leu Lys Thr Val Ala Gly  
145 150

(2) INFORMATION FOR SEQ ID NO:13:

Seq List 10-644355.txt

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 145 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Ala Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile His  
1 5 10 15  
Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe  
20 25 30  
Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu  
35 40 45  
Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu  
50 55 60  
Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Ser Gly Gly Asn Gly  
65 70 75 80  
Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe Ala  
85 90 95  
Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val  
100 105 110  
Thr Val Ala Ser Asn Leu Gln Asp Glu Leu Cys Gly Gly Leu Trp  
115 120 125  
Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr Val Ala  
130 135 140  
Gly  
145

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 155 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ala Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser Arg Leu  
1 5 10 15  
Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp Ile Thr  
20 25 30  
Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser  
35 40 45  
Ser Thr Leu Ser Gly Gly Asn Gly Ser Gly Gly Asn Gly Ser Gly Gly  
50 55 60  
Asn Gly Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp  
65 70 75 80  
Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr  
85 90 95  
Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly  
100 105 110  
Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr  
115 120 125  
Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu  
130 135 140  
Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro  
145 155

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(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Ala Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser Arg Leu  
1 5 10 15  
Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp Ile Thr  
20 25 30  
Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser  
35 40 45  
Ser Thr Leu Ser Gly Gly Asn Gly Ser Gly Gly Asn Gly Thr Gln Asp  
50 55 60  
Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile  
65 70 75 80  
Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala  
85 90 95  
Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Leu Trp Arg Leu Val  
100 105 110  
Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys  
115 120 125  
Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr  
130 135 140  
Lys Cys Ala Phe Gln Pro  
145 150

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ala Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser Arg Leu  
1 5 10 15  
Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp Ile Thr  
20 25 30  
Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser  
35 40 45  
Ser Thr Leu Ser Gly Gly Asn Gly Thr Gln Asp Cys Ser Phe Gln His  
50 55 60  
Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu Ser Asp  
65 70 75 80  
Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu Gln Asp  
85 90 95  
Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln Arg Trp  
100 105 110  
Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly Leu Leu  
115 120 125  
Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala Phe Gln

130  
Pro  
145

135

140

## (2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Ala Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln  
 1 5 10 15  
 Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly  
 20 25 30  
 Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala  
 35 40 45  
 Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser  
 50 55 60  
 Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp  
 65 70 75 80  
 Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro  
 85 90 95  
 Asp Ser Ser Thr Leu Ser Gly Gly Ser Gly Ser Gly Ser Gly Ser  
 100 105 110  
 Gly Gly Ser Gly Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser  
 115 120 125  
 Ser Asp Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln  
 130 135 140  
 Asp Tyr Pro Val Thr Val Ala Ser Asn Leu Gln  
 145 150 155

## (2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Ala Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln  
 1 5 10 15  
 Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly  
 20 25 30  
 Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala  
 35 40 45  
 Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser  
 50 55 60  
 Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp  
 65 70 75 80  
 Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro  
 85 90 95  
 Asp Ser Ser Thr Leu Ser Gly Gly Ser Gly Ser Gly Ser Gly Thr  
 100 105 110

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Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val  
115 120 125  
Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr  
130 135 140  
Val Ala Ser Asn Leu Gln  
145 150

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 145 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Ala Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp  
1 5 10 15  
Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr  
20 25 30  
Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly  
35 40 45  
Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr  
50 55 60  
Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu  
65 70 75 80  
Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu  
85 90 95  
Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu  
100 105 110  
Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg  
115 120 125  
Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Gly Gly Gly  
130 135 140  
Ser  
145

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 143 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Gly Ser Gly Gly Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser  
1 5 10 15  
Ser Asp Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln  
20 25 30  
Asp Tyr Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys  
35 40 45  
Gly Gly Leu Trp Arg Leu Val Ala Gln Arg Trp Met Glu Arg Leu  
50 55 60  
Lys Thr Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn  
65 70 75 80  
Thr Glu Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser

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85	90	95													
Cys	Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser	Arg	Leu	Leu	Gln	Glu	Thr
100	105	110													
Ser	Glu	Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	Gln	Asn	Phe
115	120	125													
Ser	Arg	Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro	Asp	Ser	Ser	Thr	Leu	
130	135	140													

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met	Ala	Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser	Ser	Asp
1	5	10	15												
Phe	Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr
20	25	30													
Pro	Val	Thr	Val	Ala	Ser	Asn	Leu	Gln	Asp	Glu	Glu	Leu	Cys	Gly	Gly
35	40	45													
Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln	Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr
50	55	60													
val	Ala	Gly	Ser	Lys	Met	Gln	Gly	Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu
65	70	75	80												
Ile	His	Phe	Val	Thr	Lys	Cys	Ala	Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu
85	90	95													
Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser	Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu
100	105	110													
Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp	Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg
115	120	125													
Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro	Asp	Ser	Ser	Thr	Leu	Gly	Gly	Gly
130	135	140													
Ser	Gly	Gly	Gly	Ser											
145															

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Gly	Ser	Gly	Gly	Gly	Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile
1	5	10	15												
Ser	Ser	Asp	Phe	Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu
20	25	30													
Gln	Asp	Tyr	Pro	Val	Thr	Val	Ala	Ser	Asn	Leu	Gln	Asp	Glu	Glu	Leu
35	40	45													
Cys	Gly	Gly	Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln	Arg	Trp	Met	Glu	Arg
50	55	60													
Leu	Lys	Thr	Val	Ala	Gly	Ser	Lys	Met	Gln	Gly	Leu	Leu	Glu	Arg	Val
65	70	75	80												

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Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro  
85 90 95  
Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu  
100 105 110  
Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn  
115 120 125  
Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu  
130 135 140

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 153 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met Ala Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp  
1 5 10 15  
Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr  
20 25 30  
Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly  
35 40 45  
Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr  
50 55 60  
Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu  
65 70 75 80  
Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu  
85 90 95  
Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu  
100 105 110  
Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg  
115 120 125  
Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Gly Gly Gly  
130 135 140  
Ser Gly Gly Ser Gly Gly Ser  
145 150

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 150 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Gly Ser Gly Gly Ser Gly Gly Ser Gly Thr Gln Asp Cys Ser  
1 5 10 15  
Phe Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu  
20 25 30  
Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn  
35 40 45  
Leu Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala  
50 55 60  
Gln Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln

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65	70	75	80												
Gly	Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile	His	Phe	Val	Thr	Lys	Cys
	85		90												95
Ala	Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile
	100		105												110
Ser	Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	Gln	Leu	Val	Ala	Leu	Lys	Pro
	115		120												125
Trp	Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys	Leu	Glu	Leu	Gln	Cys	Gln
	130		135												140
Pro	Asp	Ser	Ser	Thr	Leu										
145															

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Ala	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln
1															15
Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val	Ala	Gly	Ser	Lys	Met	Gln	Gly
	20		25												30
Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile	His	Phe	Val	Thr	Lys	Cys	Ala
	35		40												45
Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser
	50		55												60
Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp
	65		70												80
Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro
	85		90												95
Asp	Ser	Ser	Thr	Leu	Gly	Gly	Ser	Gly	Gly	Thr	Gln	Asp	Cys	Ser	
	100		105												110
Phe	Gln	His	Ser	Pro	Ile	Ser	Ser	Asp	Phe	Ala	Val	Lys	Ile	Arg	Glu
	115		120												125
Leu	Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr	Pro	Val	Thr	Val	Ala	Ser	Asn
	130		135												140
Leu	Gln														
145															

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Ala	Asp	Glu	Glu	Leu	Cys	Gly	Gly	Leu	Trp	Arg	Leu	Val	Leu	Ala	Gln
1															15
Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val	Ala	Gly	Ser	Lys	Met	Gln	Gly
	20		25												30
Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile	His	Phe	Val	Thr	Lys	Cys	Ala
	35		40												45

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Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser  
50 55 60  
Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp  
65 70 75 80  
Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro  
85 90 95  
Asp Ser Ser Thr Leu Gly Gly Ser Gly Gly Thr Gln Asp Cys  
100 105 110  
Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg  
115 120 125  
Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser  
130 135 140  
Asn Leu Gln  
145

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 150 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Ala Asp Glu Glu Leu Cys Gly Leu Trp Arg Leu Val Leu Ala Gln  
1 5 10 15  
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly  
20 25 30  
Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala  
35 40 45  
Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser  
50 55 60  
Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp  
65 70 75 80  
Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro  
85 90 95  
Asp Ser Ser Thr Leu Gly Gly Ser Gly Gly Ser Gly Gly Thr  
100 105 110  
Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe Ala val  
115 120 125  
Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr  
130 135 140  
Val Ala Ser Asn Leu Gln  
145 150

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 153 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Ala Asp Glu Glu Leu Cys Gly Leu Trp Arg Leu Val Leu Ala Gln  
1 5 10 15  
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly  
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20	25	30													
Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile	His	Phe	Val	Thr	Lys	Cys	Ala
35		40											45		
Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser
50						55				70	75	60			
Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp
65										75			80		
Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro
								85		90			95		
Asp	Ser	Ser	Thr	Leu	Gly	Gly	Gly	Ser	Gly	Gly	Ser	Gly	Gly	Gly	
								100		105			110		
Ser	Gly	Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser	Ser	Asp
								115		120			125		
Phe	Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln	Asp	Tyr
								130		135			140		
Pro	Val	Thr	Val	Ala	Ser	Asn	Leu	Gln							
								145		150					

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

1	5	10	15												
Arg	Trp	Met	Glu	Arg	Leu	Lys	Thr	Val	Ala	Gly	Ser	Lys	Met	Gln	Gly
			20			25							30		
Leu	Leu	Glu	Arg	Val	Asn	Thr	Glu	Ile	His	Phe	Val	Thr	Lys	Cys	Ala
								35		40			45		
Phe	Gln	Pro	Pro	Pro	Ser	Cys	Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile	Ser
								50		55			60		
Arg	Leu	Leu	Gln	Glu	Thr	Ser	Glu	Gln	Leu	Val	Ala	Leu	Lys	Pro	Trp
								65		70			75		80
Ile	Thr	Arg	Gln	Asn	Phe	Ser	Arg	Cys	Leu	Glu	Leu	Gln	Cys	Gln	Pro
								85		90			95		
Asp	Ser	Ser	Thr	Leu	Gly	Gly	Gly	Ser	Gly	Gly	Ser	Gly	Gly	Gly	
								100		105			110		
Ser	Gly	Gly	Thr	Gln	Asp	Cys	Ser	Phe	Gln	His	Ser	Pro	Ile	Ser	
								115		120			125		
Ser	Asp	Phe	Ala	Val	Lys	Ile	Arg	Glu	Leu	Ser	Asp	Tyr	Leu	Leu	Gln
								130		135			140		
Asp	Tyr	Pro	Val	Thr	Val	Ala	Ser	Asn	Leu	Gln					
								145		150			155		

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Seq List 10-644355.txt

Ala Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln  
1 5 10 15  
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly  
20 25 30  
Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala  
35 40 45  
Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser  
50 55 60  
Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp  
65 70 75 80  
Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro  
85 90 95  
Asp Ser Ser Thr Leu Gly Gly Ser Gly Gly Ser Gly Gly Gly  
100 105 110  
Ser Gly Gly Ser Gly Gly Ser Gly Thr Gln Asp Cys Ser Phe  
115 120 125  
Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu  
130 135 140  
Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu  
145 150 155 160  
Gln

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 155 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Ala Asp Tyr Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu  
1 5 10 15  
Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg  
20 25 30  
Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val  
35 40 45  
Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro  
50 55 60  
Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu  
65 70 75 80  
Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn  
85 90 95  
Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu  
100 105 110  
Gly Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Gly Thr  
115 120 125  
Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val  
130 135 140  
Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln  
145 150 155

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 155 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

Seq List 10-644355.txt

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Ala Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg  
1 5 10 15  
Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly  
20 25 30  
Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe  
35 40 45  
Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val  
50 55 60  
Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val  
65 70 75 80  
Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu  
85 90 95  
Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Gly Gly Ser Gly Gly  
100 105 110  
Gly Ser Gly Gly Ser Gly Gly Thr Gln Asp Cys Ser Phe Gln  
115 120 125  
His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu Ser  
130 135 140  
Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val  
145 150 155

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Ala Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr  
1 5 10 15  
Glu Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys  
20 25 30  
Leu Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser  
35 40 45  
Glu Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser  
50 55 60  
Arg Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Gly Gly  
65 70 75 80  
Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Gly Thr Gln Asp  
85 90 95  
Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile  
100 105 110  
Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala  
115 120 125  
Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val  
130 135 140  
Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr  
145 150 155

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids

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- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Ala Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile His  
1 5 10 15  
Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe  
20 25 30  
Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu  
35 40 45  
Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu  
50 55 60  
Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Gly Gly Ser Gly  
65 70 75 80  
Gly Gly Ser Gly Gly Ser Gly Gly Thr Gln Asp Cys Ser Phe  
85 90 95  
Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu  
100 105 110  
Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu  
115 120 125  
Gln Asp Glu Glu Leu Cys Gly Leu Trp Arg Leu Val Leu Ala Gln  
130 135 140  
Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly  
145 150 155

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Ala Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser Arg Leu  
1 5 10 15  
Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp Ile Thr  
20 25 30  
Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser  
35 40 45  
Ser Thr Leu Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly  
50 55 60  
Gly Gly Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp  
65 70 75 80  
Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr  
85 90 95  
Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly  
100 105 110  
Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr  
115 120 125  
Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu  
130 135 140  
Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro  
145 150 155

(2) INFORMATION FOR SEQ ID NO:36:

Seq List 10-644355.txt

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 155 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Ala Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser  
1 5 10 15  
Glu Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser  
20 25 30  
Arg Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Gly Gly  
35 40 45  
Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Thr Gln Asp  
50 55 60  
Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile  
65 70 75 80  
Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala  
85 90 95  
Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val  
100 105 110  
Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys  
115 120 125  
Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr  
130 135 140  
Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu  
145 150 155

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 155 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Ala Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val  
1 5 10 15  
Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu  
20 25 30  
Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Gly Gly Ser Gly Gly  
35 40 45  
Gly Ser Gly Gly Ser Gly Gly Thr Gln Asp Cys Ser Phe Gln  
50 55 60  
His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu Ser  
65 70 75 80  
Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu Gln  
85 90 95  
Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln Arg  
100 105 110  
Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly Leu  
115 120 125  
Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala Phe  
130 135 140  
Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln

145

150

155

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Gly Gly Gly Ser  
1

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Gly Gly Gly Ser Gly Gly Gly Ser  
1 5

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser  
1 5 10

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Ser Gly Gly Ser Gly Gly Ser  
1 5

(2) INFORMATION FOR SEQ ID NO:42:

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(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 5 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Glu Phe Gly Asn Met  
1 5

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Glu Phe Gly Gly Asn Met  
1 5

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Glu Phe Gly Gly Asn Gly Gly Asn Met  
1 5

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Gly Gly Ser Asp Met Ala Gly  
1 5

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 5 amino acids

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- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Ser Gly Gly Asn Gly  
1 5

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Ser Gly Gly Asn Gly Ser Gly Gly Asn Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Ser Gly Gly Asn Gly Ser Gly Gly Asn Gly Ser Gly Gly Asn Gly  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Ser Gly Gly Ser Gly Ser Gly Gly Ser Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Ser Gly Gly Ser Gly Ser Gly Gly Ser Gly Ser Gly  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Gly Gly Gly Ser Gly Gly  
1 5

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Gly Gly Gly Ser Gly Gly Gly  
1 5

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Gly Gly Gly Ser Gly Gly Ser Gly Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Gly Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Gly Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Gly Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser  
1 5 10 15  
Gly Gly Gly Ser Gly  
20

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CTGACCATGG CNACCCAGGA CTGCTCCTTC CAA

33

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

ACTGAAGCTT AGGGCTGACA CTGCAGCTCC AG

32

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(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

ACTGAAGCTT ACAGGGTTGA GGAGTCGGGC TG

32

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GACTGCCATG GCNACYCAGG AYTGYTCYTT YCAACACAGC CCCATC

46

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GACTGCCATG GCNACYCAGG AYTGYTCYTT YCAACACAGC CCCATC

46

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

TGTCCAACT CATCAATGTA TC

22

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

CATGGCCATG GCCGACGAGG AGCTCTGCAGG GGGCCTCT

38

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GCTAGAAGCT TACTGCAGGT TGGAGGCCAC GGTGAC

36

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

CATGGCCATG GCCTCCAAGA TGCAAGGCTT GCTGGAGC

38

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GCTAGAAGCT TACCCAGCGA CAGTCTTGAG CCGCTC

36

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

CATGGCCATG GCCCCCCCCC GCTGTCTTCG CTTCGT

36

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GCTAGAAGCT TAGGGCTGAA AGGCACATTG GGTGACA

37

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CCCTGTCTGG CGGCAACGGC ACCCAGGACT GCTCCTTCCA AC

42

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GCGGTAACGG CAGTGGAGGT AATGGCACCC AGGACTGCTC CTTCCAAC

48

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

ACGGCAGTGG TGGCAATGGG AGCGGCGGAA ATGGAACCCA GGACTGCTCC TTCCAAC

57

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GTGCCGTTGC CGCCAGACAG GGTTGAGGAG TCGGGCTG

38

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

ATTACCTCCA CTGCCGTTAC CGCCTGACAG GGTTGAGGGAG TCGGGCTG

48

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

GCTCCCATTG CCACCACTGC CGTTACCTCC AGACAGGGTT GAGGAGTCGG GCTG

54

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

GATGAGGATC CGGTGGCAAT GGGAGCGGCG GAAATGGAAC CCAGGACTGC TCCTTCCACC

60

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

GATGACGGAT CCGTTACCTC CAGACAGGGT TGAGGAGTCG GGCTG

45

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

GATGACGGAT CCGGAGGTTAA TGGCACCCAG GACTGCTCCT TCCAAC

46

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid

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- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

GACTGCCATG GCCGACGAGG AGCTCTGCG

29

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

GACTCAAGCT TACTGCAGGT TGGAGGCC

28

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

GACTCGGGAT CGGGAGGTTTC TGGCACCCAG GACTGCTCC

39

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

GACTGGGATC CGGTGGCAGT GGGAGCGGCG GATCTGGAAC C

41

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GACTTGGGAT CCACTACCTC CAGACAGGGT TGAGGGAGTC

39

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

ACTGACGGAT CCACCGCCA GGGTTGAGGA GTCGGGCTG

39

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

ACTGACGGAT CCACCTCCTG ACCCACCGCC CAGGGTTGAG GAGTCGGGCT G

51

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

ACTGACGGAT CCACCTCCTG ACCCACCTCC TGACCCACCG CCCAGGGTTG AGGAGTCGGG  
CTG

60  
63

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

ACGTAAAGCT TACAGGGTTG AGGAGTCG

28

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GTCAGTGGAT CCGGAGGTAC CCAGGACTGC TCCTTCCAAC

40

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(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GTCAGTGGAT CCGGAGGTGG CACCCAGGAC TGCTCCTTCC AAC

43

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GTCAGTGGAT CCGGAGGTGG CTCAGGGGGA GGTAGTGGTA CCCAGGACTG CTCCTTCCAC

60

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

GTTGCCATGG CNTCNAAYCT GCARGAYGAR GARCTGTGCG GGGGCCTCTG GCGGCTG

57

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GTTGCCATGG CNAAYCTGCA RGAYGARGAR CTGTGYGGGG GCCTCTGGCG GCTGGTC

57

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

GTTGCCATGG CNCTGCARGA YGARGARCTG TGYGGYGGCC TCTGGCGGCT GGTCTTG

57

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GTTGCCATGG CNCARGAYGA RGARCTGTGY GGYGGYCTCT GGCAGCTGGT CCTGGCA

57

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

GTTGCCATGG CNGAYGARGA RCTGTGYGGY GGYCTCTGGC GGCTGGTCCT GGCACAG

57

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GTTGCCATGG CNGARGARCT GTGYGGYGGY CTCTGGCGGC TGGTCCTGGC ACAGCGC

57

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GTTGCCATGG CNGARCTGTG YGGYGGYCTG TGGCGYCTGG TCCTGGCACA GCGCTGG

57

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

GTTGCCATGG CNCTGTGYGG YGGYCTGTGG CGYCTGGTCC TGGCACAGCG CTGGATG

57

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

TATGCAAGCT TAGGCCACGG TGACTGGGTA

30

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

TATGCAAGCT TAGGAGGCCA CGGTGACTGG

30

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

TATGCAAGCT TAGTTGGAGG CCACGGTGAC

30

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TATGCAAGCT TACAGGTTGG AGGCCACGGT

30

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

TATGCAAGCT TACTGCAGGT TGGAGGCCAC

30

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

TATGCAAGCT TAGTCCTGCA GGTTGGAGGC

30

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

TATGCAAGCT TACTCGTCCT GCAGGTTGGA

30

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

TATGCAAGCT TACTCCTCGT CCTGCAGGTT

30

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GCCACCCAGG	ACTGCTCCTT	CCAACACAGC	CCCATCTCCT	CCGACTTCGC	TGTAAAATC	60
CGTGAGCTGT	CTGACTACCT	GCTTCAAGAT	TACCCAGTCA	CCGTGGCCTC	CAACCTGCAG	120
GACGAGGAGC	TCTGCGGGGC	GCTCTGGCGG	CTGGTCCTGG	CACAGCGCTG	GATGGAGCGG	180
CTCAAGACTG	TCGCTGGTC	CAAGATGCAA	GGCTTGCTGG	AGCGCGTGAA	CACGGAGATA	240
CACTTTGTCA	CCAAATGTGC	CTTTCAAGCC	CCCCCCAGCT	GTCTTCGCTT	CGTCCAGACC	300
AACATCTCCC	GCCTCCTGCA	GGAGACCTCC	GAGCAGCTGG	TGGCGCTGAA	GCCCTGGATC	360
ACTCGCCAGA	ACTTCTCCCG	GTGCCTGGAG	CTGCAGTGTC	AGCCCC		405

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(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

GCCACCCAGG	ACTGCTCCTT	CCAACACAGC	CCCATCTCCT	CCGACTTCGC	TGTAAAATC	60
CGTGAGCTGT	CTGACTACCT	GCTTCAAGAT	TACCCAGTCA	CCGTGGCCTC	CAACCTGCAG	120
GACGAGGAGC	TCTGCGGGGG	CCTCTGGCGG	CTGGTCCCTGG	CACAGCGCTG	GATGGAGCGG	180
CTCAAGACTG	TCGCTGGGTC	CAAGATGCAA	GGCTTGCTGG	AGCGCGTGAA	CACGGAGATA	240
CACTTTGTCA	CCAAATGTGC	CTTTCAGCCC	CCCCCCAGCT	GTCTTCGCTT	CGTCCAGACC	300
AACATCTCCC	GCCTCCTGCA	GGAGACCTCC	GAGCAGCTGG	TGGCGCTGAA	GCCCTGGATC	360
ACTGCCAGA	ACTTCTCCCG	GTGCCTGGAG	CTGCAGTGTC	AGCCCGACTC	CTCAACCCCTG	420

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GCCACCCAGG	ACTGCTCCTT	CCAACACAGC	CCCATCTCCT	CCGACTTCGC	TGTAAAATC	60
CGTGAGCTGT	CTGACTACCT	GCTTCAAGAT	TACCCAGTCA	CCGTGGCCTC	CAACCTGCAG	120
GACGAGGAGC	TCTGCGGGGG	CCTCTGGCGG	CTGGTCCCTGG	CACAGCGCTG	GATGGAGCGG	180
CTCAAGACTG	TCGCTGGGTC	CAAGATGCAA	GGCTTGCTGG	AGCGCGTGAA	CACGGAGATA	240
CACTTTGTCA	CCAAATGTGC	CTTTCAGGAG	ACCTCCGAGC	AGCTGGTGGC	GCTGAAGCCC	300
TGGATCACTC	GCCAGAACTT	CTCCCGGTGC	CTGGAGCTGC	AGTGTCAAGCC	CGACTCCTCA	360
ACCCCTG						366

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

GGAACCTCAGG	ATTGTTCTTT	CCAACACAGC	CCCATCTCCT	CCGACTTCGC	TGTAAAATC	60
CGTGAGCTGT	CTGACTACCT	GCTTCAAGAT	TACCCAGTCA	CCGTGGCCTC	CAACCTGCAG	120
GACGAGGAGC	TCTGCGGGGG	CCTCTGGCGG	CTGGTCCCTGG	CACAGCGCTG	GATGGAGCGG	180
CTCAAGACTG	TCGCTGGGTC	CAAGATGCAA	GGCTTGCTGG	AGCGCGTGAA	CACGGAGATA	240
CACTTTGTCA	CCAAATGTGC	CTTTCAGCCC	CCCCCCAGCT	GTCTTCGCTT	CGTCCAGACC	300
AACATCTCCC	GCCTCCTGCA	GGAGACCTCC	GAGCAGCTGG	TGGCGCTGAA	GCCCTGGATC	360
ACTGCCAGA	ACTTCTCCCG	GTGCCTGGAG	CTGCAGTGTC	AGCCC		405

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid

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(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GGTACCCAGG	ATTGTTCTTT	CCAACACAGC	CCCATCTCCT	CCGACTTCGC	TGTAAAATC	60
CGTGAGCTGT	CTGACTACCT	GCTTCAAGAT	TACCCAGTCA	CCGTGGCCTC	CAACCTGCAG	120
GACGAGGAGC	TCTGCGGGGG	CCTCTGGCGG	CTGGTCTCTGG	CACAGCGCTG	GATGGAGCGG	180
CTCAAGACTG	TCGCTGGGTC	CAAGATGCAA	GGCTTGTGG	AGCGCGTGAA	CACGGAGATA	240
CACTTGTCA	CCAAATGTGC	CTTTCAGCCC	CCCCCCAGCT	GTCTTCGCTT	CGTCCAGACC	300
AACATCTCCC	GCCTCTGCA	GGAGACCTCC	GAGCAGCTGG	TGGCGCTGAA	GCCCTGGATC	360
ACTGCCAGA	ACTTCTCCCG	GTGCCTGGAG	CTGCAGTGT	AGCCCGACTC	CTCAACCTG	420

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 405 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

GCCACTCAGG	ACTGTTCTTT	CCAACACAGC	CCCATCTCCT	CCGACTTCGC	TGTAAAATC	60
CGTGAGCTGT	CTGACTACCT	GCTTCAAGAT	TACCCAGTCA	CCGTGGCCTC	CAACCTGCAG	120
GACGAGGAGC	TCTGCGGGGG	CCTCTGGCGG	CTGGTCTCTGG	CACAGCGCTG	GATGGAGCGG	180
CTCAAGACTG	TCGCTGGGTC	CAAGATGCAA	GGCTTGTGG	AGCGCGTGAA	CACGGAGATA	240
CACTTGTCA	CCAAATGTGC	CTTTCAGCCC	CCCCCCAGCT	GTCTTCGCTT	CGTCCAGACC	300
AACATCTCCC	GCCTCTGCA	GGAGACCTCC	GAGCAGCTGG	TGGCGCTGAA	GCCCTGGATC	360
ACTGCCAGA	ACTTCTCCCG	GTGCCTGGAG	CTGCAGTGT	AGCCC		405

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 420 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

GCCACTCAGG	ACTGCTCTTT	TCAACACAGC	CCCATCTCCT	CCGACTTCGC	TGTAAAATC	60
CGTGAGCTGT	CTGACTACCT	GCTTCAAGAT	TACCCAGTCA	CCGTGGCCTC	CAACCTGCAG	120
GACGAGGAGC	TCTGCGGGGG	CCTCTGGCGG	CTGGTCTCTGG	CACAGCGCTG	GATGGAGCGG	180
CTCAAGACTG	TCGCTGGGTC	CAAGATGCAA	GGCTTGTGG	AGCGCGTGAA	CACGGAGATA	240
CACTTGTCA	CCAAATGTGC	CTTTCAGCCC	CCCCCCAGCT	GTCTTCGCTT	CGTCCAGACC	300
AACATCTCCC	GCCTCTGCA	GGAGACCTCC	GAGCAGCTGG	TGGCGCTGAA	GCCCTGGATC	360
ACTGCCAGA	ACTTCTCCCG	GTGCCTGGAG	CTGCAGTGT	AGCCCGACTC	CTCAACCTG	420

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 465 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

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GCCGACGAGG	AGCTCTGCGG	GGGCCTCTGG	CGGCTGGTCC	TGGCACAGCG	CTGGATGGAG	60
CGGCTCAAGA	CTGTCGCTGG	GTCCAAGATG	CAAGGCTTGC	TGGAGCGCGT	GAACACGGAG	120
ATACACTTGT	TCACCAAATG	TGCCCTTCAG	CCCCCCCCCA	GCTGTCTTCG	CTTCGTCCAG	180
ACCAACATCT	CCCGCCTCCT	GCAGGGAGACC	TCCGAGCAGC	TGGTGGCGCT	GAAGCCCTGG	240
ATCACTCGCC	AGAACTTCTC	CCGGTGCCTG	GAGCTGCAGT	GTCAGCCCAG	CTCCTCAACC	300
CTGTCTGGAG	GTAACGGATC	CGGTGGCAAT	GGGAGCGCG	GAAATGGAAC	CCAGGACTGC	360
TCCTTCCAAC	ACAGCCCCAT	CTCCTCCGAC	TTCGCTGTCA	AAATCCGTGA	GCTGTCTGAC	420
TACCTGCTTC	AAGATTACCC	AGTCACCGTG	GCCTCCAACC	TGCAG		465

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

GCCGACGAGG	AGCTCTGCGG	GGGCCTCTGG	CGGCTGGTCC	TGGCACAGCG	CTGGATGGAG	60
CGGCTCAAGA	CTGTCGCTGG	GTCCAAGATG	CAAGGCTTGC	TGGAGCGCGT	GAACACGGAG	120
ATACACTTGT	TCACCAAATG	TGCCCTTCAG	CCCCCCCCCA	GCTGTCTTCG	CTTCGTCCAG	180
ACCAACATCT	CCCGCCTCCT	GCAGGGAGACC	TCCGAGCAGC	TGGTGGCGCT	GAAGCCCTGG	240
ATCACTCGCC	AGAACTTCTC	CCGGTGCCTG	GAGCTGCAGT	GTCAGCCCAG	CTCCTCAACC	300
CTGTCTGGCG	GTAACGGCAG	TGGAGGTAAT	GGCACCCAGG	ACTGCTCCTT	CCAACACAGC	360
CCCATCTCCT	CCGACTTCGC	TGTCAAATC	CGTGAGCTGT	CTGACTACCT	GCTTCAAGAT	420
TACCCAGTCA	CCGTGGCCTC	CAACCTGCAG				450

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GCCGACGAGG	AGCTCTGCGG	GGGCCTCTGG	CGGCTGGTCC	TGGCACAGCG	CTGGATGGAG	60
CGGCTCAAGA	CTGTCGCTGG	GTCCAAGATG	CAAGGCTTGC	TGGAGCGCGT	GAACACGGAG	120
ATACACTTGT	TCACCAAATG	TGCCCTTCAG	CCCCCCCCCA	GCTGTCTTCG	CTTCGTCCAG	180
ACCAACATCT	CCCGCCTCCT	GCAGGGAGACC	TCCGAGCAGC	TGGTGGCGCT	GAAGCCCTGG	240
ATCACTCGCC	AGAACTTCTC	CCGGTGCCTG	GAGCTGCAGT	GTCAGCCCAG	CTCCTCAACC	300
CTGTCTGGCG	GCAACGGCAC	CCAGGACTGC	TCCCTCCAAC	ACAGCCCCAT	CTCCTCCGAC	360
TTCGCTGTCA	AAATCCGTGA	GCTGTCTGAC	TACCTGCTTC	AAGATTACCC	AGTCACCGTG	420
GCCTCCAACC	TGCAG					435

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

GCCTCCAAGA	TGCAAGGCTT	GCTGGAGCGC	GTGAACACGG	AGATACACTT	TGTCACCAAA	60
TGTGCTTTC	AGCCCCCCCC	CAGCTGTCTT	CGCTTCGTCC	AGACCAACAT	CTCCCGCCTC	120
CTGCAGGAGA	CCTCCGAGCA	GCTGGTGGCG	CTGAAGCCAT	GGATCACTCG	CCAGAACTTC	180

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TCCCGGTGCC	TGGAGCTGCA	GTGTCAGCCC	GACTCCTCAA	CCCTGTCTGG	AGGTAACGGA	240
TCCGGTGGCA	ATGGGAGCGG	CGGAAATGGA	ACCCAGGACT	GCTCCTTCCA	ACACAGCCCC	300
ATCTCCTCCG	ACTTCGCTGT	CAAATCCGT	GAGCTGTCTG	ACTACCTGCT	TCAAGATTAC	360
CCAGTCACCG	TGGCCTCAA	CCTGCAGGAC	GAGGAGCTCT	GCGGGGGCCT	CTGGCGGCTG	420
GTCCTGGCAC	AGCGCTGGAT	GGAGCGGCTC	AAGACTGTGCG	CTGGG		465

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

GCCTCCAAGA	TGCAAGGCTT	GCTGGAGCGC	GTGAACACGG	AGATACACTT	TGTCACCAAA	60
TGTGCCCTTC	AGCCCCCCCC	CAGCTGTCTT	CGCTTCGTCC	AGACCAACAT	CTCCCGCCTC	120
CTGCAGGAGA	CCTCCGAGCA	GCTGGTGGCG	CTGAAGCCCT	GGATCACTCG	CCAGAACTTC	180
TCCCGGTGCC	TGGAGCTGCA	GTGTCAGCCC	GACTCCTCAA	CCCTGTCTGG	AGGTAACGGA	240
TCCGGAGGTA	ATGGCACCCA	GGACTGCTCC	TTCCAACACA	GCCCCATCTC	CTCCGACTTC	300
GCTGTAAAAA	TCCGTGAGCT	GTCTGACTAC	CTGCTTCAG	ATTACCCAGT	CACCGTGGCC	360
TCCAACCTGC	AGGACGAGGA	GCTCTGCGGG	GGCCTCTGGC	GGCTGGTCCT	GGCACAGCGC	420
TGGATGGAGC	GGCTCAAGAC	TGTCGCTGGG				450

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

GCCTCCAAGA	TGCAAGGCTT	GCTGGAGCGC	GTGAACACGG	AGATACACTT	TGTCACCAAA	60
TGTGCCCTTC	AGCCCCCCCC	CAGCTGTCTT	CGCTTCGTCC	AGACCAACAT	CTCCCGCCTC	120
CTGCAGGAGA	CCTCCGAGCA	GCTGGTGGCG	CTGAAGCCCT	GGATCACTCG	CCAGAACTTC	180
TCCCGGTGCC	TGGAGCTGCA	GTGTCAGCCC	GACTCCTCAA	CCCTGTCTGG	CGGCAACGGC	240
ACGCAGGACT	GCTCCTTCA	ACACAGCCCC	ATCTCCTCCG	ACTTCGCTGT	CAAATCCGT	300
GAGCTGTCTG	ACTACCTGCT	TCAAGATTAC	CCAGTCACCG	TGGCCTCAA	CCTGCAGGAC	360
GAGGAGCTCT	GCGGGGGCCT	CTGGCGGCTG	GTCCTGGCAC	AGCGCTGGAT	GGAGCGGCTC	420
AAGACTGTGCG	CTGGG					435

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

GCCCCCCCCA	GCTGTCTTCG	CTTCGTCCAG	ACCAACATCT	CCCGCCTCCT	GCAGGAGACC	60
TCCGAGCAGC	TGGTGGCGCT	GAAGCCCTGG	ATCACTCGCC	AGAACTTCTC	CCGGTGCCTG	120
GAGCTGCACT	GTCAGCCCGA	CTCCTCAACC	CTGTCTGGAG	GTAACGGCAG	TGGTGGCAAT	180
GGGAGCGGTG	GAAATGGAAC	CCAGGACTGC	TCCCTCCAAC	ACAGCCCCAT	CTCCTCCGAC	240
TTCGCTGTCA	AAATCCGTGA	GCTGTCTGAC	TACCTGCTTC	AAGATTACCC	AGTCACCGTG	300
GCCTCCAACC	TGCAGGACGA	GGAGCTCTGC	GGGGGCCCTC	GGCGGCTGGT	CCTGGCACAG	360

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CGCTGGATGG AGCGGCTCAA GACTGTCGCT GGGTCCAAGA TGCAAGGCTT GCTGGAGCGC	420
GTGAACACGG AGATACACTT TGTACCAAA TGTGCCTTC AGCCC	465

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

GCCCCCCCCA GCTGTCTTCG CTTCGTCCAG ACCAACATCT CCCGCCTCCT GCAGGGAGACC	60
TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG ATCACTCGCC AGAACCTCTC CCGGTGCCTG	120
GAGCTGCAGT GTCAGCCCGA CTCCCTCAACC CTGTCAGGCG GTAACGGCAG TGGAGGTAAT	180
GGCACCCAGG ACTGCTCCTT CCAACACAGC CCCATCTCCT CCGACTTCGC TGTCAAAATC	240
CGTGAGCTGT CTGACTACCT GCTTCAAGAT TACCCAGTCA CCGTGGCCTC CAACCTGCAG	300
GACGAGGAGC TCTGCGGGGG CCTCTGGCGG CTGGTCTCTGG CACAGCGCTG GATGGAGCGG	360
CTCAAGACTG TCGCTGGTC CAAGATGCAA GGCTTGCTGG AGCGCGTGAA CACGGAGATA	420
CACTTGTCA CCAAATGTGC CTTTCAGCCC	450

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

GCCCCCCCCA GCTGTCTTCG CTTCGTCCAG ACCAACATCT CCCGCCTCCT GCAGGGAGACC	60
TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG ATCACTCGCC AGAACCTCTC CCGGTGCCTG	120
GAGCTGCAGT GTCAGCCCGA CTCCCTCAACC CTGTCAGGCG GCAACGGCAC GCAGGACTGC	180
TCCTTCCAAC ACAGCCCCAT CTCCCTCCGAC TTGCTGTCA AAATCCGTGA GCTGTCTGAC	240
TACCTGCTTC AAGATTACCC AGTCACCGTG GCCTCCAACC TGCAAGGACGA GGAGCTCTGC	300
GGGGGCCTCT GGCAGCTGGT CCTGGCACAG CGCTGGATGG AGCGGCTCAA GACTGTGCT	360
GGGTCCAAGA TGCAAGGCTT GCTGGAGCGC GTGAACACGG AGATACACTT TGTCACCAAA	420
TGTGCCTTTC AGCCC	435

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

GCCGACGAGG AGCTCTGCGG GGGCCTCTGG CGGCTGGTCC TGGCACAGCG CTGGATGGAG	60
CGGCTCAAGA CTGTCGCTGG GTCCAAGATG CAAGGCTTGC TGGAGCGCGT GAACACGGAG	120
ATACACTTTG TCACCAAATG TGCCTTTCAG CCCCCCCCCA GCTGTCTTCG CTTCGTCCAG	180
ACCAACATCT CCCGCCTCCT GCAGGAGACC TCCGAGCAGC TGGTGGCGCT GAAGCCCTGG	240
ATCACTCGCC AGAACCTCTC CCGGTGCCTG GAGCTGCAGT GTCAGCCCGA CTCCCTCAACC	300
CTGTCAGGAG GTAGTGGATC CGGAGGTTCT GGCAACCCAG GACTGCTCCT TCCAACACAG	360
CCCCATCTCC TCCGACTTCG CTGTCAAAT CCGTGAGCTG TCTGACTACC TGCTTCAAGA	420
TTACCCAGTC ACCGTGGCCT CCAACCTGCA G	451

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(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

GGCGACGAGG	AGCTCTGCGG	GGGCCTCTGG	CGGCTGGTCC	TGGCACAGCG	CTGGATGGAG	60
CGGCTCAAGA	CTGTCGCTGG	GTCCAAGATG	CAAGGCTTGC	TGGAGCGCGT	GAACACGGAG	120
ATACACTTTG	TCACCAAATG	TGCCCTTCAG	CCCCCCCCCA	GCTGTCTTCG	CTTCGTCCAG	180
ACCAACATCT	CCCGCCTCCT	GCAGGAGACC	TCCGAGCAGC	TGGTGGCGCT	GAAGCCCTGG	240
ATCACTCGCC	AGAACTTCTC	CCGGTGCCTG	GAGCTGCAGT	GTCAGCCCGA	CTCCTCAACC	300
CTGTCTGGAG	GTAGTGGATC	CGGTGGCAGT	GGGAGCGGCG	GATCTGGAAC	CCAGGACTGC	360
TCCTTCCAAC	ACAGCCCCAT	CTCCTCCGAC	TTCGCTGTCA	AAATCCGTGA	GCTGTCTGAC	420
TACCTGCTTC	AAGATTACCC	AGTCACCGTG	GCCTCCAACC	TGCAG		465

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

CCATGGCCAC	CCAGGACTGC	TCCTTCCAAC	ACAGCCCCAT	CTCCTCCGAC	TTCGCTGTCA	60
AAATCCGTGA	GCTGTCTGAC	TACCTGCTTC	AAGATTACCC	AGTCACCGTG	GCCTCCAACC	120
TGCAGGACGA	GGAGCTCTGC	GGGGGCCTCT	GGCGGCTGGT	CCTGGCACAG	CGCTGGATGG	180
AGCGGCTCAA	GACTGTCGCT	GGGTCCAAGA	TGCAAGGCTT	GCTGGAGCGC	GTGAACACGG	240
AGATACACTT	TGTCAACAAA	TGTGCTTTTC	AGCCCCCCCC	CAGCTGTCTT	CGCTTCGTCC	300
AGACCAACAT	CTCCCGCCTC	CTGCAGGAGA	CCTCCGAGCA	GCTGGTGGCG	CTGAAGCCCT	360
GGATCACTCG	CCAGAACTTC	TCCCCGGTGCC	TGGAGCTGCA	GTGTCAGCCC	GACTCCTCAA	420
CCCTGGGCGG	TGGATCC					437

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 436 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

GGATCCGGAG	GTACCCAGGA	CTGCTCTTC	CAACACAGCC	CCATCTCCTC	CGACTTCGCT	60
GTCAAATCC	GTGAGCTGTC	TGACTACCTG	CTTCAAGATT	ACCCAGTCAC	CGTGGCCTCC	120
AACCTGCAGG	ACGAGGAGCT	CTGGGGGGC	CTCTGGCGC	TGGTCTTGGC	ACAGCGCTGG	180
ATGGAGCGGC	TCAAGACTGT	CGCTGGGTCC	AAGATGCAAG	GCTTGCTTGA	GCGCGTGAAC	240
ACGGAGATAC	ACTTTGTAC	CAAATGTGCC	TTTCAGCCCC	CCCCCAGCTG	TCTTCGCTTC	300
GTCCAGACCA	ACATCTCCCG	CCTCCTGCAG	GAGACCTCCG	AGCAGCTGGT	GGCGCTGAAG	360
CCCTGGATCA	CTCGCCAGAA	CTTCTCCCGG	TGCCTGGAGC	TGCAGTGTCA	GCCCCGACTCC	420
TCAACCCCTGT	AAGCTT					436

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 449 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

CCATGGCCAC	CCAGGACTGC	TCCTTCAAC	ACAGCCCCAT	CTCCTCCGAC	TTCGCTGTCA	60
AAATCCGTGA	GCTGCTGAC	TACCTGCTTC	AAGATTACCC	AGTCACCGTG	GCCTCCAACC	120
TGCAGGACGA	GGAGCTCTGC	GGGGGCCTCT	GGCGGCTGGT	CCTGGCACAG	CGCTGGATGG	180
AGCGGCTCAA	GACTGTGCT	GGGTCCAAGA	TGCAAGGCTT	GCTGGAGCGC	GTGAACACGG	240
AGATACACTT	TGTCACCAAA	TGTGCTTTT	AGCCCCCCCC	CAGCTGTCTT	CGCTTCGTCC	300
AGACCAACAT	CTCCCGCTC	CTGCAGGAGA	CCTCCGAGCA	GCTGGTGGCG	CTGAAGCCCT	360
GGATCACTCG	CCAGAACCTC	TCCCGGTGCC	TGGAGCTGCA	GTGTCAGCCC	GACTCCTCAA	420
CCCTGGCGG	TGGGTAGGA	GGTGGATCC				449

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 439 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

GGATCCGGAG	GTGGCACCCA	GGACTGCTCC	TTCCAACACA	GCCCCATCTC	CTCCGACTTC	60
GCTGTCAAAA	TCCGTGAGCT	GTCTGACTAC	CTGCTTCAG	ATTACCCAGT	CACCGTGGCC	120
TCCAACCTGC	AGGACGAGGA	GCTCTCGGG	GGCCTCTGGC	GGCTGGTCCT	GGCACAGCGC	180
TGGATGGAGC	GGCTCAAGAC	TGTCGCTGGG	TCCAAGATGC	AAGGTTGCT	GGAGCGCGTG	240
AACACGGAGA	TACACTTTGT	CACCAATGT	GCCTTCAGC	CCCCCCCCAG	CTGTCTTCGC	300
TTCGTCCAGA	CCAACATCTC	CCGCCTCCTG	CAGGAGACCT	CCGAGCAGCT	GGTGGCGCTG	360
AAGCCCTGGA	TCACTCGCCA	GAACTTCTCC	CGGTGCCTGG	AGCTGCAGTG	TCAGCCCGAC	420
TCCTCAACCC	TGTAAGCTT					439

(2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

CCATGGCCAC	CCAGGACTGC	TCCTTCAAC	ACAGCCCCAT	CTCCTCCGAC	TTCGCTGTCA	60
AAATCCGTGA	GCTGCTGAC	TACCTGCTTC	AAGATTACCC	AGTCACCGTG	GCCTCCAACC	120
TGCAGGACGA	GGAGCTCTGC	GGGGGCCTCT	GGCGGCTGGT	CCTGGCACAG	CGCTGGATGG	180
AGCGGCTCAA	GACTGTGCT	GGGTCCAAGA	TGCAAGGCTT	GCTGGAGCGC	GTGAACACGG	240
AGATACACTT	TGTCACCAAA	TGTGCTTTT	AGCCCCCCCC	CAGCTGTCTT	CGCTTCGTCC	300
AGACCAACAT	CTCCCGCTC	CTGCAGGAGA	CCTCCGAGCA	GCTGGTGGCG	CTGAAGCCCT	360
GGATCACTCG	CCAGAACCTC	TCCCGGTGCC	TGGAGCTGCA	GTGTCAGCCC	GACTCCTCAA	420
CCCTGGCGG	TGGGTAGGA	GGTGGTCAG	GAGGTGGATC	C		461

(2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 457 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

GGATCCGGAG	GTGGCTCAGG	GGGAGGTAGT	GGTACCCAGG	ACTGCTCCTT	CCAACACAGC	60
CCCATCTCCT	CCGACTTCGC	TGTAAAATC	CGTGAGCTGT	CTGACTACCT	GCTTCAAGAT	120
TACCCAGTCA	CCGTGGCCTC	CAACCTGCAG	GACGAGGAGC	TCTGCGGGGG	CCTCTGGCGG	180
CTGGTCTGG	CACAGCGCTG	GATGGAGCGG	CTCAAGACTG	TCGCTGGGTC	CAAGATGCAA	240
GGCTTGCTGG	AGCGCGTGA	CACGGAGATA	CACTTTGTCA	CCAAATGTGC	CTTTCAGCCC	300
CCCCCCAGCT	GTCTCGCTT	CGTCCAGACC	AACATCTCCC	GCCTCCTGCA	GGAGACCTCC	360
GAGCAGCTGG	TGGCGCTGAA	GCCCTGGATC	ACTGCCAGA	ACTTCTCCG	GTGCCTGGAG	420
CTGCAGTGTC	AGCCCGACTC	CTCAACCCCTG	TAAGCTT			457

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 438 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

GCCGACGAGG	AGCTCTGCGG	GGGCCTCTGG	CGGCTGGTCC	TGGCACAGCG	CTGGATGGAG	60
CGGCTCAAGA	CTGTCGCTGG	GTCCAAGATG	CAAGGCTTGC	TGGAGCGCGT	GAACACGGAG	120
ATACACTTTG	TCACCAAATG	TGCCCTTCAG	CCCCCCCCCA	GCTGTCTTCG	CTTCGTCCAG	180
ACCAACATCT	CCCGCCTCCT	GCAGGAGACC	TCCGAGCAGC	TGGTGGCGCT	GAAGCCCTGG	240
ATCACTCGCC	AGAACTTCTC	CCGGTGCCTG	GAGCTGCAGT	GTCAGCCCAG	CTCCTCAACC	300
CTGGCGGTG	GATCCGGAGG	TACCCAGGAC	TGCTCCTTCC	AACACAGCCC	CATCTCCTCC	360
GACTTCGCTG	TCAAAATCCG	TGAGCTGTCT	GACTACCTGC	TTCAAGATTA	CCCAAGTCACC	420
GTGGCCTCCA	ACCTGCAG					438

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

GCCGACGAGG	AGCTCTGCGG	GGGCCTCTGG	CGGCTGGTCC	TGGCACAGCG	CTGGATGGAG	60
CGGCTCAAGA	CTGTCGCTGG	GTCCAAGATG	CAAGGCTTGC	TGGAGCGCGT	GAACACGGAG	120
ATACACTTTG	TCACCAAATG	TGCCCTTCAG	CCCCCCCCCA	GCTGTCTTCG	CTTCGTCCAG	180
ACCAACATCT	CCCGCCTCCT	GCAGGAGACC	TCCGAGCAGC	TGGTGGCGCT	GAAGCCCTGG	240
ATCACTCGCC	AGAACTTCTC	CCGGTGCCTG	GAGCTGCAGT	GTCAGCCCAG	CTCCTCAACC	300
CTGGCGGTG	GATCCGGAGG	TGGCACCCAG	GACTGCTCCT	TCCAACACAG	CCCCATCTCC	360
TCCGACTTCG	CTGTAAAAT	CCGTGAGCTG	TCTGACTACC	TGCTTCAAGA	TTACCCAGTC	420
ACCGTGGCCT	CCAACCTGCA	G				441

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

GCCGACGAGG	AGCTCTGCGG	GGGCCTCTGG	CGGCTGGTCC	TGGCACAGCG	CTGGATGGAG	60
CGGCTCAAGA	CTGTCGCTGG	GTCCAAGATG	CAAGGCTTGC	TGGAGCGCGT	GAACACGGAG	120
ATACACTTTG	TCACCAAATG	TGCCCTTCAG	CCCCCCCCCA	GCTGTCTTCG	CTTCGTCCAG	180
ACCAACATCT	CCCGCCTCCT	GCAGGAGACC	TCCGAGCAGC	TGGTGGCGCT	GAAGCCCTGG	240
ATCACTCGCC	AGAACTTCTC	CCGGTGCCTG	GAGCTGCAGT	GTCAGCCCCGA	CTCCTCAACC	300
CTGGCGGTG	GGTCAGGAGG	TGGATCCGGA	GGTACCCAGG	ACTGCTCCTT	CCAACACAGC	360
CCCATCTCCT	CCGACTTCGC	TGTCAAATC	CGTGAGCTGT	CTGACTACCT	GCTTCAAGAT	420
TACCCAGTCA	CCGTGGCCTC	CAACCTGCAG				450

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

GCCGACGAGG	AGCTCTGCGG	GGGCCTCTGG	CGGCTGGTCC	TGGCACAGCG	CTGGATGGAG	60
CGGCTCAAGA	CTGTCGCTGG	GTCCAAGATG	CAAGGCTTGC	TGGAGCGCGT	GAACACGGAG	120
ATACACTTTG	TCACCAAATG	TGCCCTTCAG	CCCCCCCCCA	GCTGTCTTCG	CTTCGTCCAG	180
ACCAACATCT	CCCGCCTCCT	GCAGGAGACC	TCCGAGCAGC	TGGTGGCGCT	GAAGCCCTGG	240
ATCACTCGCC	AGAACTTCTC	CCGGTGCCTG	GAGCTGCAGT	GTCAGCCCCGA	CTCCTCAACC	300
CTGGCGGTG	GATCCGGAGG	TGGTCAGGG	GGAGGTTAGTG	GTACCCAGGA	CTGCTCCTTC	360
CAACACAGCC	CCATCTCCTC	CGACTTCGCT	GTCAAATC	GTGAGCTGTC	TGACTACCTG	420
CTTCAAGATT	ACCCAGTCAC	CGTGGCCTCC	AAACCTGCAG			459

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

GCCGACGAGG	AGCTCTGCGG	GGGCCTCTGG	CGGCTGGTCC	TGGCACAGCG	CTGGATGGAG	60
CGGCTCAAGA	CTGTCGCTGG	GTCCAAGATG	CAAGGCTTGC	TGGAGCGCGT	GAACACGGAG	120
ATACACTTTG	TCACCAAATG	TGCCCTTCAG	CCCCCCCCCA	GCTGTCTTCG	CTTCGTCCAG	180
ACCAACATCT	CCCGCCTCCT	GCAGGAGACC	TCCGAGCAGC	TGGTGGCGCT	GAAGCCCTGG	240
ATCACTCGCC	AGAACTTCTC	CCGGTGCCTG	GAGCTGCAGT	GTCAGCCCCGA	CTCCTCAACC	300
CTGGCGGTG	GGTCAGGAGG	TGGTCAGGG	GGTGGATCCG	GAGGTGGCAC	CCAGGACTGC	360
TCCTTCAAC	ACAGCCCCAT	CTCCTCCGAC	TTCGCTGTCA	AAATCCGTGA	GCTGTCTGAC	420
TACCTGCTTC	AAGATTACCC	AGTCACCGTG	GCCTCCAACC	TGCAG		465

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

GCCGACGAGG	AGCTCTGCGG	GGGCCTCTGG	CGGCTGGTCC	TGGCACAGCG	CTGGATGGAG	60
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CGGCTCAAGA	CTGTCGCTGG	GTCCAAGATG	CAAGGCTTGC	TGGAGCGCGT	GAACACGGAG	120
ATACACTTTG	TCACCAAATG	TGCCCTTCAG	CCCCCCCCCA	GCTGCCTTCG	CTTCGTCCAG	180
ACCAACATCT	CCCGCCTCCT	GCAGGAGACC	TCCGAGCAGC	TGGTGGCGCT	GAAGCCCTGG	240
ATCACTCGCC	AGAACTTCTC	CCGGTGCCTG	GAGCTGCAGT	GTCAGCCCAG	CTCCTCAACC	300
CTGGGCGGTG	GGTCAGGAGG	TGGTCAGGA	GGTGGATCCG	GAGGTGGCTC	AGGGGGAGGT	360
AGTGGTACCC	AGGACTGCTC	CTTCCAACAC	AGCCCCATCT	CCTCCGACTT	CGCTGTCAAA	420
ATCCGTGAGC	TGTCTGACTA	CCTGCTTCAA	GATTACCCAG	TCACCGTGGC	CTCCAACCTG	480
		CAG				483

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

GCCGATTACC	CAGTCACCGT	GGCCTCAAAC	CTGCAGGACG	AGGAGCTCTG	CGGGGGCCTC	60
TGGCGGCTGG	TCCTGGCACA	GCGCTGGATG	GAGCGGCTCA	AGACTGTCGC	TGGGTCCAAG	120
ATGCAAGGCT	TGCTGGAGCG	CGTGAACACG	GAGATACACT	TTGTCACCAA	ATGTGCCTTT	180
CAGCCCCCCC	CCAGCTGTCT	TCGCTTCGTC	CAGACCAACA	TCTCCCGCCT	CCTGCAGGAG	240
ACCTCCGAGC	AGCTGGTGGC	GCTGAAGCCC	TGGATCACTC	GCCAGAACTT	CTCCCGGTGC	300
CTGGAGCTGC	AGTGTCAAGC	CGACTCCTCA	ACCCCTGGCG	GTGGGTCAAGG	AGGTGGGTCA	360
GGAGGTGGAT	CCGGAGGTGG	CACCCAGGAC	TGCTCCTTCC	AACACAGCCC	CATCTCCTCC	420
GAATTCGCTG	TCAAAATCCG	TGAGCTGTCT	GAATACCTGC	TTCAA		465

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

GCCGCCTCCA	ACCTGCAGGA	CGAGGAGCTC	TGCGGGGCC	TCTGGCGGCT	GGTCCTGGCA	60
CAGCGCTGGA	TGGAGCGCT	CAAGACTGTC	GCTGGTCCA	AGATGCAAGG	CTTGCTGGAG	120
CGCGTGAACA	CGGAGATACA	CTTTGTCA	AAATGTGCCT	TTCAGCCCCC	CCCCAGCTGT	180
CTTCGCTTCG	TCCAGACCAA	CATCTCCCGC	CTCCTGCAGG	AGACCTCCGA	GCAGCTGGTG	240
GCGCTGAAGC	CCTGGATCAC	TCGCCAGAAC	TTCTCCCGGT	GCCGGAGCT	GCAGTGTCA	300
CCCGACTCCT	CAACCCCTGG	CGGTGGTCA	GGAGGTGGGT	CAGGAGGTGG	ATCCGGAGGT	360
GGCACCCAGG	ACTGCTCCTT	CCAAACACAGC	CCCATCTCCT	CCGACTTCGC	TGTCAAATC	420
CGTGAGCTGT	CTGACTACCT	GCTTCAAGAT	TACCCAGTCA	CCGTG		465

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

GCCGTCGCTG	GGTCCAAGAT	GCAAGGCTTG	CTGGAGCGCG	TGAACACGGA	GATACACTTT	60
GTCACCAAAT	GTGCTTTCA	CCCCCCCCCA	AGCTGTCTTC	GCTTCGTCCA	GACCAACATC	120
TCCCGCTCC	TGCAGGAGAC	CTCCGAGCAG	CTGGTGGCGC	TGAAGCCCTG	GATCACTCGC	180

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CAGAACTTCT	CCCGGTGCCT	GGAGCTGCAG	TGTCAGCCG	ACTCCTCAAC	CCTGGGCGGT	240
GGGTCAAGGAG	GTGGGTCAGG	AGGTGGATCC	GGAGGTGGCA	CCCAGGACTG	CTCCTTCAA	300
CACAGCCCCA	TCTCCTCCGA	CTTCGCTGTC	AAAATCCGTG	AGCTGTCTGA	CTACCTGCTT	360
CAAGATTACC	CAGTCACCGT	GGCCTCCAAC	CTGCAGGACG	AGGAGCTCTG	CGGGGGCCTC	420
TGGCGGCTGG	TCCTGGACAC	CGCCTGGATG	GAGCGGCTCA	AGACT		465

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GCCTCCAAGA	TGCAAGGCTT	GCTGGAGCGC	GTGAACACGG	AGATAACACTT	TGTCACCAAA	60
TGTGCCCTTC	AGCCCCCCCC	CAGCTGTCTT	CGCTTCGTCC	AGACCAACAT	CTCCCGCCTC	120
CTGCAGGAGA	CCTCCGAGCA	GCTGGTGGCG	CTGAAGCCCT	GGATCACTCG	CCAGAACTTC	180
TCCCGGTGCC	TGGAGCTGCA	GTGTCAAGCCC	GAECTCCTCAA	CCCTGGGCGG	TGGGTCAAGGA	240
GGTGGGTCAG	GAGGTGGATC	CGGAGGTGGC	ACCCAGGACT	GCTCCTTCCA	ACACAGCCCC	300
ATCTCCTCCG	ACTTCGCTGT	CAAATCCGT	GAGCTGTCTG	ACTACCTGCT	TCAAGATTAC	360
CCAGTCACCG	TGGCCTCCAA	CCTGCAGGAC	GAGGAGCTCT	GCGGGGGCCT	CTGGCGGCTG	420
GTCCTGGCAC	AGCGCTGGAT	GGAGCGGCTC	AAGACTGTGCG	CTGGG		465

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

GCCCCCCCCA	GCTGTCTTCG	CTTCGTCCAG	ACCAACATCT	CCCGCCTCCT	GCAGGGAGACC	60
TCCGAGCAGC	TGGTGGCGCT	GAAGCCCTGG	ATCACTCGCC	AGAACTTCTC	CCGGTGCCTG	120
GAGCTGCAGT	GTCAGCCCGA	CTCCTCAACC	CTGGGCGGTG	GGTCAGGAGG	TGGGTCAAGGA	180
GGTGGATCCG	GAGGTGGCAC	CCAGGACTGC	TCCTTCCAAC	ACAGCCCCAT	CTCCTCCGAC	240
TTCGCTGTCA	AAATCCGTGA	GCTGTCTGAC	TACCTGCTTC	AAGATTACCC	AGTCACCGTG	300
GCCTCCAACC	TGCAGGACGA	GGAGCTCTGC	GGGGGCCTCT	GGCGGCTGGT	CCTGGCACAG	360
CGCTGGATGG	AGCGGCTCAA	GACTGTGCGT	GGGTCCAAGA	TGCAAGGCTT	GCTGGAGCGC	420
GTGAACACGG	AGATAACACTT	TGTCAACAAA	TGTGCCTTTC	AGCCCC		465

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GCCCGCTTCG	TCCAGACCAA	CATCTCCCGC	CTCCTGCAGG	AGACCTCCGA	GCAGCTGGTG	60
GCGCTGAAGC	CCTGGATCAC	TCGCCAGAAC	TTCTCCCGT	GCCTGGAGCT	GCAGTGTCA	120
CCCGACTCCT	CAACCCCTGGG	CGGTGGGTCA	GGAGGTGGGT	CAGGAGGTGG	ATCCGGAGGT	180
GGCACCCAGG	ACTGCTCCTT	CCAACACAGC	CCCATCTCCT	CCGACTTCGC	TGTCAAAATC	240
CGTGAGCTGT	CTGACTACCT	GCTTCAAGAT	TACCCAGTCA	CCGTGGCCTC	CAACCTGCAG	300
GACGAGGAGC	TCTGCGGGGG	CCTCTGGCGG	CTGGTCCTGG	CACAGCGCTG	GATGGAGCGG	360

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CTCAAGACTG TCGCTGGTC CAAGATGCAA GGCTTGCTGG AGCGCGTGAA CACGGAGATA	420
CACTTGTCA CCAAATGTGC CTTTCAGCCC CCCCCCAGCT GTCTT	465

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

GCCACCAACA TCTCCCGCCT CCTGCAGGAG ACCTCCGAGC AGCTGGTGGC GCTGAAGCCC	60
TGGATCACTC GCCAGAACCTT CTCCCGGTGC CTGGAGCTGC AGTGTCAAGCC CGACTCCTCA	120
ACCCTGGGCG GTGGGTCAAGG AGGTGGGTCA GGAGGTGGAT CCGGAGGTGG CACCCAGGAC	180
TGCTCCTTCC AACACAGCCC CATCTCCTCC GACTTCGCTG TCAAAATCCG TGAGCTGTCT	240
GACTACCTGC TTCAAGATTA CCCAGTCACC GTGGCCTCCA ACCTGCAGGA CGAGGAGCTC	300
TGCGGGGGCC TCTGGCGGCT GGTCCCTGGCA CAGCGCTGGA TGGAGCGGCT CAAGACTGTC	360
GCTGGGTCCA AGATGCAAGG CTTGCTGGAG CGCGTGAACA CGGAGATACA CTTTGTCAACC	420
AAATGTGCCT TTCAGCCCCC CCCCAGCTGT CTTCGCTTCG TCCAG	465

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe Ala	
1 5 10 15	
Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val	
20 25 30	
Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp	
35 40 45	
Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr Val Ala	
50 55 60	
Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile His	
65 70 75 80	
Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Ser Cys Leu Arg Phe	
85 90 95	
Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu	
100 105 110	
Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu	
115 120 125	
Glu Leu Gln Cys Gln Pro	
130	

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe Ala  
1 5 10 15  
Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val  
20 25 30  
Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp  
35 40 45  
Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr Val Ala  
50 55 60  
Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile His  
65 70 75 80  
Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Ser Cys Leu Arg Phe  
85 90 95  
Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu  
100 105 110  
Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu  
115 120 125  
Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu  
130 135

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 209 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp Phe Ala  
1 5 10 15  
Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val  
20 25 30  
Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp  
35 40 45  
Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr Val Ala  
50 55 60  
Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu Ile His  
65 70 75 80  
Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Ser Cys Leu Arg Phe  
85 90 95  
Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu  
100 105 110  
Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu  
115 120 125  
Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser  
130 135 140  
Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala Pro Gln Pro Pro Leu  
145 150 155 160  
Leu Leu Leu Leu Leu Pro Val Gly Leu Leu Leu Ala Ala Ala  
165 170 175  
Trp Cys Leu His Trp Gln Arg Thr Arg Arg Arg Thr Pro Arg Pro Gly  
180 185 190  
Glu Gln Val Pro Pro Val Pro Ser Pro Gln Asp Leu Leu Leu Val Glu  
195 200 205  
His

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(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

ACCCAGGACT	GCTCCTTCCA	ACACAGCCCC	ATCTCCTCCG	ACTTCGCTGT	CAAATCCGT	60
GAGCTGTCTG	ACTACCTGCT	TCAAGATTAC	CCAGTCACCG	TGGCCTCCAA	CCTGCAGGAC	120
GAGGAGCTCT	GCGGGGGCCCT	CTGGCGGCTG	GTCCTGGCAC	AGCGCTGGAT	GGAGCGGCTC	180
AAGACTGTCTG	CTGGGTCCAA	GATGCAAGGC	TTGCTGGAGC	GCGTGAACAC	GGAGATACAC	240
TTTGTACCA	AATGTGCCTT	TCAGCCCCCC	CCCAGCTGTC	TTCGCTTCGT	CCAGACCAAC	300
ATCTCCCGCC	TCCTGCAGGA	GACCTCCGAG	CAGCTGGTGG	CGCTGAAGCC	CTGGATCACT	360
CGCCAGAACT	TCTCCCGGTG	CCTGGAGCTG	CAGTGTCAAGC	CC		402

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 630 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

ACCCAGGACT	GCTCCTTCCA	ACACAGCCCC	ATCTCCTCCG	ACTTCGCTGT	CAAATCCGT	60
GAGCTGTCTG	ACTACCTGCT	TCAAGATTAC	CCAGTCACCG	TGGCCTCCAA	CCTGCAGGAC	120
GAGGAGCTCT	GCGGGGGCCCT	CTGGCGGCTG	GTCCTGGCAC	AGCGCTGGAT	GGAGCGGCTC	180
AAGACTGTCTG	CTGGGTCCAA	GATGCAAGGC	TTGCTGGAGC	GCGTGAACAC	GGAGATACAC	240
TTTGTACCA	AATGTGCCTT	TCAGCCCCCC	CCCAGCTGTC	TTCGCTTCGT	CCAGACCAAC	300
ATCTCCCGCC	TCCTGCAGGA	GACCTCCGAG	CAGCTGGTGG	CGCTGAAGCC	CTGGATCACT	360
CGCCAGAACT	TCTCCCGGTG	CCTGGAGCTG	CAGTGTCAAGC	CCGACTCCTC	AACCCTGCCA	420
CCCCCATGGA	GTCCCCGGCC	CCTGGAGGCC	ACAGCCCCGA	CAGCCCCGCA	GCCCCCTCTG	480
CTCCTCCTAC	TGCTGCTGCC	CGTGGGCCTC	CTGCTGCTGG	CCGCTGCCCTG	GTGCCTGCAC	540
TGGCAGAGGA	CGCGCGGAG	GACACCCCGC	CCTGGGGAGC	AGGTGCCCTCC	CGTCCCCAGT	600
CCCCAGGACC	TGCTGTTGT	GGAGCACTGA				630

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser
1			5			10			15		
Gly	Gly	Gly	Ser	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly
			20			25					

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid

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- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

Pro Pro Pro Trp Ser Pro Arg Pro Leu Gly Ala Thr Ala  
1 5 10 15  
Gly Gln Pro Pro Leu  
20

(2) INFORMATION FOR SEQ ID NO:150:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

Pro Pro Pro Trp Ser Pro Arg Pro Leu Gly Ala Thr Ala Pro Thr  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:151:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

Val Glu Thr Val Phe His Arg Val Ser Gln Asp Gly Leu Leu Thr Ser  
1 5 10 15